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RAW SEQUENCE LISTING

DATE: 07/27/2001

PATENT APPLICATION: US/09/823,069

TIME: 11:04:27

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\07272001\I823069.raw

ENTERED

3 <110> APPLICANT: Wheeler, Kenneth
 4 Mach, Robert
 5 Childers, Steven
 6 Shelness, Gregory
 7 Wang, Li-Ming
 9 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS UTILIZING AN ALTERNATIVE SPLICE
 VARIANT OF THE
 10 SIGMA-1 RECEPTOR
 12 <130> FILE REFERENCE: 9151.6
 14 <140> CURRENT APPLICATION NUMBER: 09/823,069
 15 <141> CURRENT FILING DATE: 2001-03-30
 17 <150> PRIOR APPLICATION NUMBER: US 60/193,694
 18 <151> PRIOR FILING DATE: 2000-03-31
 20 <160> NUMBER OF SEQ ID NOS: 6
 22 <170> SOFTWARE: PatentIn version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 579
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(579)
 33 <400> SEQUENCE: 1
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 36 1 5 10 15
 38 gct gtc gca gcg gtg ctg acc cag gtc gtc tgg ctc tgg ctg ggt acg 96
 39 Ala Val Ala Ala Val Leu Thr Gln Val Val Trp Leu Trp Leu Gly Thr
 40 20 25 30
 42 cag agc ttc gtc ttc cag cgc gaa gag ata gcg cag ttg gcg cgg cag 144
 43 Gln Ser Phe Val Phe Gln Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
 44 35 40 45
 46 tac gct ggg ctg gac cac gag ctg gcc ttc tct cgt ctg atc gtg gag 192
 47 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu
 48 50 55 60
 50 ctg cgg cgg ctg cac cca ggc cac gtg ctg ccc gac gag gag ctg cag 240
 51 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
 52 65 70 75 80
 54 tgg gtg ttc gtg aat gcg ggt ggc tgg atg ggc gcc atg tgc ctt ctg 288
 55 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Leu Leu
 56 85 90 95
 58 cac gcc tcg ctg tcc gag tat gtg ctg ctc ttc ggc acc gcc ttg ggc 336
 59 His Ala Ser Leu Ser Glu Tyr Val Leu Phe Gly Thr Ala Leu Gly
 60 100 105 110
 62 tcc cgc gcc cac tcg ggg gag acg gta gta cac ggg cct ggt gag gca 384
 63 Ser Arg Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala
 64 115 120 125
 66 aca gct gtg gag tgg ggg cca aac aca tgg atg gtg gag tac ggc cgg 432

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68      130      135      140
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71 Gly Val Ile Pro Ser Thr Leu Ala Phe Ala Leu Ala Asp Thr Val Phe
72 145      150      155      160
74 agc acc cag gac ttc ctc acc ctc ttc tat act ctt cgc tcc tat gct      528
75 Ser Thr Gln Asp Phe Leu Thr Leu Phe Tyr Thr Leu Arg Ser Tyr Ala
76      165      170      175
78 cgg ggc ctc cgg ctt gag ctc acc acc tac ctc ttt ggc cag gac cct      576
79 Arg Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Pro
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86 <211> LENGTH: 192
87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
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96 Ala Val Ala Ala Val Leu Thr Gln Val Val Trp Leu Trp Leu Gly Thr
97      20      25      30
100 Gln Ser Phe Val Phe Gln Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
101      35      40      45
104 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu
105      50      55      60
108 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
109 65      70      75      80
112 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Leu Leu
113      85      90      95
116 His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly
117      100      105      110
120 Ser Arg Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala
121      115      120      125
124 Thr Ala Val Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg
125      130      135      140
128 Gly Val Ile Pro Ser Thr Leu Ala Phe Ala Leu Ala Asp Thr Val Phe
129 145      150      155      160
132 Ser Thr Gln Asp Phe Leu Thr Leu Phe Tyr Thr Leu Arg Ser Tyr Ala
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141 <211> LENGTH: 579
142 <212> TYPE: DNA
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145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(579)
149 <400> SEQUENCE: 3

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151 Met Pro Trp Ala Ala Gly Arg Arg Trp Ala Trp Ile Thr Leu Ile Leu
152 1          5          10          15
154 act att atc gca gtg ctg atc cag gcc gcc tgg ttg tgg ctg ggc act      96
155 Thr Ile Ile Ala Val Leu Ile Gln Ala Ala Trp Leu Trp Leu Gly Thr
156          20          25          30
158 caa aac ttc gtc ttc tct aga gaa gaa ata gcg cag ctt gct cga cag      144
159 Gln Asn Phe Val Phe Ser Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
160          35          40          45
162 tat gcg ggg ctg gac cat gag ctt gcc ttc tct cgg ctg atc gtg gag      192
163 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu
164          50          55          60
166 ctg cgg agg ctg cac cca ggc cac gtg ctg ccg gat gag gag ctg cag      240
167 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
168 65          70          75          80
170 tgg gta ttt gtg aac gcg ggc ggc tgg atg ggc gcc atg tgt att ctg      288
171 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Ile Leu
172          85          90          95
174 cac gcc tcg ctg tct gag tac gtg ctg ctc ttc ggc acc gcc ctg ggc      336
175 His Ala Ser Leu Ser Glu Tyr Val Leu Phe Gly Thr Ala Leu Gly
176          100          105          110
178 tcc cat ggc cat tcg gga gag aca gtt gta cac ggg cct gga gaa gca      384
179 Ser His Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala
180          115          120          125
182 acg gct ctg gag tgg gga cca aac acg tgg atg gtg gag tac ggc cgg      432
183 Thr Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg
184          130          135          140
186 ggt gtt att ccg tct acc ctg ttc ttt gca cta gcc gac acc ttc ttc      480
187 Gly Val Ile Pro Ser Thr Leu Phe Phe Ala Leu Ala Asp Thr Phe Phe
188 145          150          155          160
190 ggc acc cag gac tac ctc aca ctc ttc tat acc ctt cgg gcc tat gcc      528
191 Gly Thr Gln Asp Tyr Leu Thr Leu Phe Tyr Thr Leu Arg Ala Tyr Ala
192          165          170          175
194 cgg ggc ctc cgg ctt gag ctt acc acc tac ctc ttt ggc caa gac tcc      576
195 Arg Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Ser
196          180          185          190
198 tga      579
201 <210> SEQ ID NO: 4
202 <211> LENGTH: 192
203 <212> TYPE: PRT
204 <213> ORGANISM: Mus musculus
206 <400> SEQUENCE: 4
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209 1          5          10          15
212 Thr Ile Ile Ala Val Leu Ile Gln Ala Ala Trp Leu Trp Leu Gly Thr
213          20          25          30
216 Gln Asn Phe Val Phe Ser Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
217          35          40          45
220 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu

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221      50                      55                      60
224 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
225 65                      70                      75                      80
228 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Ile Leu
229                      85                      90                      95
232 His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly
233                      100                      105                      110
236 Ser His Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala
237                      115                      120                      125
240 Thr Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg
241                      130                      135                      140
244 Gly Val Ile Pro Ser Thr Leu Phe Phe Ala Leu Ala Asp Thr Phe Phe
245 145                      150                      155                      160
248 Gly Thr Gln Asp Tyr Leu Thr Leu Phe Tyr Thr Leu Arg Ala Tyr Ala
249                      165                      170                      175
252 Arg Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Ser
253                      180                      185                      190

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256 <210> SEQ ID NO: 5

257 <211> LENGTH: 31

258 <212> TYPE: DNA

259 <213> ORGANISM: Artificial Sequence

261 <220> FEATURE:

262 <221> NAME/KEY: misc_feature

263 <222> LOCATION: (1)..(31)

264 <223> OTHER INFORMATION: Synthetic Oligonucleotide Primer.

267 <400> SEQUENCE: 5

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272 <211> LENGTH: 31

273 <212> TYPE: DNA

274 <213> ORGANISM: Artificial Sequence

276 <220> FEATURE:

277 <221> NAME/KEY: misc_feature

278 <222> LOCATION: (1)..(31)

279 <223> OTHER INFORMATION: Synthetic Oligonucleotide Primer.

282 <400> SEQUENCE: 6

283 taacggtacc tcaggagtct tggccaaaga g

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VERIFICATION SUMMARY

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